

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/001,227

DATE: 12/10/2001

TIME: 15:00:38

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\12102001\I001227.raw

ENTERED

4 <110> APPLICANT: KAPPELLER-LIBERMANN
 5 SILOS-SANTIAGO
 7 <120> TITLE OF INVENTION: METHODS OF USING 18903 TO TREAT PAIN AND
 8 PAIN-RELATED DISORDERS
 10 <130> FILE REFERENCE: MNI-199
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/001,227
 C--> 12 <141> CURRENT FILING DATE: 2001-11-30
 12 <150> PRIOR APPLICATION NUMBER: 60/250929
 13 <151> PRIOR FILING DATE: 2000-11-30
 15 <160> NUMBER OF SEQ ID NOS: 7
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1983
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (98)...(1849)
 28 <400> SEQUENCE: 1
 29 ccttttagcca attcgccga ggcctccgc cccagtactt gctggcaggg attaagagca 60
 30 gataaaagtg tgctcacaca ctgtagacac ggctacc atg cca tcc aca gtg ttg 115
 31 Met Pro Ser Thr Val Leu
 32 1 5
 34 cca tcc aca gtg ttg cca tca ctc ctg ccc aca gca gga gct ggc tgg 163
 35 Pro Ser Thr Val Leu Pro Ser Leu Leu Pro Thr Ala Gly Ala Gly Trp
 36 10 15 20
 38 agc atg agg tgg att ctg tgc tgg agc ctc acc ctc tgc ctg atg gcg 211
 39 Ser Met Arg Trp Ile Leu Cys Trp Ser Leu Thr Leu Cys Leu Met Ala
 40 25 30 35
 42 cag acg gcc ttg ggt gcc ttg cac acc aag agg cct caa gtg gtc acc 259
 43 Gln Thr Ala Leu Gly Ala Leu His Thr Lys Arg Pro Gln Val Val Thr
 44 40 45 50
 46 aaa tat gga acc ctg caa gga aaa cag atg cat gtg ggg aag aca ccc 307
 47 Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met His Val Gly Lys Thr Pro
 48 55 60 65 70
 50 atc caa gtc ttt tta gga gtc ccc ttc tcc aga cct cct cta ggt atc 355
 51 Ile Gln Val Phe Leu Gly Val Pro Phe Ser Arg Pro Pro Leu Gly Ile
 52 75 80 85
 54 ctc agg ttt gca cct cca gaa ccc ccg gag ccc tgg aaa gga atc aga 403
 55 Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu Pro Trp Lys Gly Ile Arg
 56 90 95 100
 58 gat gct acc acc tac ccg cct ggg tgc ctg cag gag tcc tgg ggc cag 451
 59 Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu Gln Glu Ser Trp Gly Gln
 60 105 110 115
 62 ctg gcc tcg atg tac gtc agc acg cgg gaa cgg tac aag tgg ctg cgc 499
 63 Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg Tyr Lys Trp Leu Arg
 64 120 125 130

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66 ttc agc gag gac tgt ctg tac ctg aac gtg tac gcg ccg gcg cgc gcg 547
67 Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val Tyr Ala Pro Ala Arg Ala
68 135 140 145 150
70 ccc ggg gat ccc cag ctg cca gtg atg gtc tgg ttc ccg gga ggc gcc 595
71 Pro Gly Asp Pro Gln Leu Pro Val Met Val Trp Phe Pro Gly Gly Ala
72 155 160 165
74 ttc atc gtg ggc gct gct tct tcg tac gag ggc tct gac ttg gcc gcc 643
75 Phe Ile Val Gly Ala Ala Ser Ser Tyr Glu Gly Ser Asp Leu Ala Ala
76 170 175 180
78 cgc gag aaa gtg gtg ctg gtg ttt ctg cag cac agg ctc ggc atc ttc 691
79 Arg Glu Lys Val Val Leu Val Phe Leu Gln His Arg Leu Gly Ile Phe
80 185 190 195
82 ggc ttc ctg agc acg gac gac agc cac gcg cgc ggg aac tgg ggg ctg 739
83 Gly Phe Leu Ser Thr Asp Asp Ser His Ala Arg Gly Asn Trp Gly Leu
84 200 205 210
86 ctg gac cag atg gcg gct ctg cgc tgg gtg cag gag aac atc gca gcc 787
87 Leu Asp Gln Met Ala Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala
88 215 220 225 230
90 ttc ggg gga gac cca gga aat gtg acc ctg ttc ggc cag tcg gcg ggg 835
91 Phe Gly Gly Asp Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly
92 235 240 245
94 gcc atg agc atc tca gga ctg atg atg tca ccc cta gcc tcg ggt ctc 883
95 Ala Met Ser Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu
96 250 255 260
98 ttc cat cgg gcc att tcc cag agt ggc acc gcg tta ttc aga ctt ttc 931
99 Phe His Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe
100 265 270 275
102 atc act agt aac cca ctg aaa gtg gcc aag aag gtt gcc cac ctg gct 979
103 Ile Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala
104 280 285 290
106 gga tgc aac cac aac agc aca cag atc ctg gta aac tgc ctg agg gca 1027
107 Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg Ala
108 295 300 305 310
110 cta tca ggg acc aag gtg atg cgt gtg tcc aac aag atg aga ttc ctc 1075
111 Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg Phe Leu
112 315 320 325
114 caa ctg aac ttc cag aga gac ccg gaa gag att atc tgg tcc atg agc 1123
115 Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp Ser Met Ser
116 330 335 340
118 cct gtg gtg gat ggt gtg gtg atc cca gat gac cct ttg gtg ctc ctg 1171
119 Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro Leu Val Leu Leu
120 345 350 355
122 acc cag ggg aag gtt tca tct gtg ccc tac ctt cta ggt gtc aac aac 1219
123 Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu Leu Gly Val Asn Asn
124 360 365 370
126 ctg gaa ttc aat tgg ctc ttg cct tat atc atg aag ttc ccg cta aac 1267
127 Leu Glu Phe Asn Trp Leu Leu Pro Tyr Ile Met Lys Phe Pro Leu Asn
128 375 380 385 390
130 cgg cag gcg atg aga aag gaa acc atc act aag atg ctc tgg agt acc 1315

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131 Arg Gln Ala Met Arg Lys Glu Thr Ile Thr Lys Met Leu Trp Ser Thr
132          395          400          405
134 cgc acc ctg ttg aat atc acc aag gag cag gta cca ctt gtg gtg gag 1363
135 Arg Thr Leu Leu Asn Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu
136          410          415          420
138 gag tac ctg gac aat gtc aat gag cat gac tgg aag atg cta cga aac 1411
139 Glu Tyr Leu Asp Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn
140          425          430          435
142 cgt atg atg gac ata gtt caa gat gcc act ttc gtg tat gcc aca ctg 1459
143 Arg Met Met Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu
144          440          445          450
146 cag act gct cac tac cac cga gat gcc ggc ctc cct gtc tac ctg tat 1507
147 Gln Thr Ala His Tyr His Arg Asp Ala Gly Leu Pro Val Tyr Leu Tyr
148 455          460          465          470
150 gaa ttt gag cac cac gct cgt gga ata atc gtc aaa ccc cgc act gat 1555
151 Glu Phe Glu His His Ala Arg Gly Ile Ile Val Lys Pro Arg Thr Asp
152          475          480          485
154 ggg gca gac cat ggg gat gag atg tac ttc ctc ttt ggg ggc ccc ttc 1603
155 Gly Ala Asp His Gly Asp Glu Met Tyr Phe Leu Phe Gly Gly Pro Phe
156          490          495          500
158 gcc aca ggc ctt tcc atg ggt aag gag aag gca ctt agc ctc cag atg 1651
159 Ala Thr Gly Leu Ser Met Gly Lys Glu Lys Ala Leu Ser Leu Gln Met
160          505          510          515
162 atg aaa tac tgg gcc aac ttt gcc cgc aca gga aac ccc aat gat ggg 1699
163 Met Lys Tyr Trp Ala Asn Phe Ala Arg Thr Gly Asn Pro Asn Asp Gly
164          520          525          530
166 aat ctg ccc tgc tgg cca cgc tac aac aag gat gaa aag tac ctg cag 1747
167 Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys Asp Glu Lys Tyr Leu Gln
168 535          540          545          550
170 ctg gat ttt acc aca aga gtg ggc atg aag ctc aag gag aag aag atg 1795
171 Leu Asp Phe Thr Thr Arg Val Gly Met Lys Leu Lys Glu Lys Lys Met
172          555          560          565
174 gct ttt tgg atg agt ctg tac cag tct caa aga cct gag aag cag agg 1843
175 Ala Phe Trp Met Ser Leu Tyr Gln Ser Gln Arg Pro Glu Lys Gln Arg
176          570          575          580
178 caa ttc taagggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc 1899
179 Gln Phe
182 caggccctgg ggagactagc catggacata cctggggaca agagttctac ccaagggcga 1959
183 attcgtttaa acctgcagga ctg
185 <210> SEQ ID NO: 2 1983
186 <211> LENGTH: 584
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 2
191 Met Pro Ser Thr Val Leu Pro Ser Thr Val Leu Pro Ser Leu Leu Pro
192 1          5          10          15
193 Thr Ala Gly Ala Gly Trp Ser Met Arg Trp Ile Leu Cys Trp Ser Leu
194          20          25          30
195 Thr Leu Cys Leu Met Ala Gln Thr Ala Leu Gly Ala Leu His Thr Lys

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```

196          35          40          45
197 Arg Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
198          50          55          60
199 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe Ser
200 65          70          75          80
201 Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
202          85          90          95
203 Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu
204          100          105          110
205 Gln Glu Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu
206          115          120          125
207 Arg Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val
208          130          135          140
209 Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met Val
210 145          150          155          160
211 Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser Tyr Glu
212          165          170          175
213 Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val Phe Leu Gln
214          180          185          190
215 His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp Asp Ser His Ala
216          195          200          205
217 Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala Ala Leu Arg Trp Val
218          210          215          220
219 Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp Pro Gly Asn Val Thr Leu
220 225          230          235          240
221 Phe Gly Gln Ser Ala Gly Ala Met Ser Ile Ser Gly Leu Met Met Ser
222          245          250          255
223 Pro Leu Ala Ser Gly Leu Phe His Arg Ala Ile Ser Gln Ser Gly Thr
224          260          265          270
225 Ala Leu Phe Arg Leu Phe Ile Thr Ser Asn Pro Leu Lys Val Ala Lys
226          275          280          285
227 Lys Val Ala His Leu Ala Gly Cys Asn His Asn Ser Thr Gln Ile Leu
228          290          295          300
229 Val Asn Cys Leu Arg Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser
230 305          310          315          320
231 Asn Lys Met Arg Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu
232          325          330          335
233 Ile Ile Trp Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp
234          340          345          350
235 Asp Pro Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr
236          355          360          365
237 Leu Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Ile
238          370          375          380
239 Met Lys Phe Pro Leu Asn Arg Gln Ala Met Arg Lys Glu Thr Ile Thr
240 385          390          395          400
241 Lys Met Leu Trp Ser Thr Arg Thr Leu Leu Asn Ile Thr Lys Glu Gln
242          405          410          415
243 Val Pro Leu Val Val Glu Glu Tyr Leu Asp Asn Val Asn Glu His Asp
244          420          425          430

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245 Trp Lys Met Leu Arg Asn Arg Met Met Asp Ile Val Gln Asp Ala Thr
246          435          440          445
247 Phe Val Tyr Ala Thr Leu Gln Thr Ala His Tyr His Arg Asp Ala Gly
248          450          455          460
249 Leu Pro Val Tyr Leu Tyr Glu Phe Glu His His Ala Arg Gly Ile Ile
250 465          470          475          480
251 Val Lys Pro Arg Thr Asp Gly Ala Asp His Gly Asp Glu Met Tyr Phe
252          485          490          495
253 Leu Phe Gly Gly Pro Phe Ala Thr Gly Leu Ser Met Gly Lys Glu Lys
254          500          505          510
255 Ala Leu Ser Leu Gln Met Met Lys Tyr Trp Ala Asn Phe Ala Arg Thr
256          515          520          525
257 Gly Asn Pro Asn Asp Gly Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys
258          530          535          540
259 Asp Glu Lys Tyr Leu Gln Leu Asp Phe Thr Thr Arg Val Gly Met Lys
260 545          550          555          560
261 Leu Lys Glu Lys Lys Met Ala Phe Trp Met Ser Leu Tyr Gln Ser Gln
262          565          570          575
263 Arg Pro Glu Lys Gln Arg Gln Phe
264          580
267 <210> SEQ ID NO: 3
268 <211> LENGTH: 1752
269 <212> TYPE: DNA
270 <213> ORGANISM: Homo sapiens
272 <220> FEATURE:
273 <221> NAME/KEY: CDS
274 <222> LOCATION: (1)...(1752)
276 <400> SEQUENCE: 3
277 atg cca tcc aca gtg ttg cca tcc aca gtg ttg cca tca ctc ctg ccc 48
278 Met Pro Ser Thr Val Leu Pro Ser Thr Val Leu Pro Ser Leu Leu Pro
279 1 5 10 15
281 aca gca gga gct ggc tgg agc atg agg tgg att ctg tgc tgg agc ctc 96
282 Thr Ala Gly Ala Gly Trp Ser Met Arg Trp Ile Leu Cys Trp Ser Leu
283 20 25 30
285 acc ctc tgc ctg atg gcg cag acg gcc ttg ggt gcc ttg cac acc aag 144
286 Thr Leu Cys Leu Met Ala Gln Thr Ala Leu Gly Ala Leu His Thr Lys
287 35 40 45
289 agg cct caa gtg gtc acc aaa tat gga acc ctg caa gga aaa cag atg 192
290 Arg Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
291 50 55 60
293 cat gtg ggg aag aca ccc atc caa gtc ttt tta gga gtc ccc ttc tcc 240
294 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe Ser
295 65 70 75 80
297 aga cct cct cta ggt atc ctc agg ttt gca cct cca gaa ccc ccg gag 288
298 Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
299 85 90 95
301 ccc tgg aaa gga atc aga gat gct acc acc tac ccg cct ggg tgc ctg 336
302 Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu
303 100 105 110

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5